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Reviewer: Keisha Douglas

Timestamp: [year=2008; month=10; day=3; hr=15; min=50; sec=21; ms=531;]

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Application No:10595388

Version No:1.0

Input Set:

Output Set:

Started:2008-09-02 18:55:23.355

Finished:2008-09-02 18:55:23.981

Elapsed:0 hr(s) 0 min(s) 0 sec(s) 626 ms

Total Warnings:4

Total Errors:0

No. of SeqIDs Defined:20

Actual SeqID Count:20

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)

SEQUENCE LISTING

<110> Istituto Superiore di Sanita
National Institutes of Health
Robbins, Paul
Rosenberg, Steven
Maccalli, Cristina

<120> COLORECTAL ANTIGEN

<130> 134-03

<140> 10595388

<141> 2008-09-02

<150> US 60/512,040

<151> 2003-10-15

<160> 20

<170> PatentIn version 3.5

<210> 1

<211> 1413

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (85)..(1395)

<220>

<221> misc_feature

<222> (1180)..(1240)

<223> nucleotide sequence encoding the immunogenic peptide

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cctgcatccc atgactcgga gctg atg gcc ttc atg acg agg aag ttg tgg 111

Met Ala Phe Met Thr Arg Lys Leu Trp

1

5

gac ctg gag cag cag gtg aag gcc cag act gat gag ata ctg tcc aag 159

Asp Leu Glu Gln Gln Val Lys Ala Gln Thr Asp Glu Ile Leu Ser Lys

10

15

20

25

gat cag aag ata gcg gcc cta gag gac ctg gtg cag acc ctc cgg cca 207

Asp Gln Lys Ile Ala Ala Leu Glu Asp Leu Val Gln Thr Leu Arg Pro

30

35

40

cac cca gcc gag gca acc ctg cag cgg cag gag gaa ctg gag acg atg 255

His Pro Ala Glu Ala Thr Leu Gln Arg Gln Glu Glu Leu Glu Thr Met

45

50

55

tgt gtg cag ctg cag cgg cag gtc agg gag atg gag cgg ttc ctc agt	303
Cys Val Gln Leu Gln Arg Gln Val Arg Glu Met Glu Arg Phe Leu Ser	
60 65 70	
gac tat ggc ctg cag tgg gtg ggc gag ccc atg gac cag gag gac tca	351
Asp Tyr Gly Leu Gln Trp Val Gly Glu Pro Met Asp Gln Glu Asp Ser	
75 80 85	
gag agc aag aca gtc tca gag cat ggc gag agg gac tgg atg aca gcc	399
Glu Ser Lys Thr Val Ser Glu His Gly Glu Arg Asp Trp Met Thr Ala	
90 95 100 105	
aag aag ttc tgg aag cca ggg gac tca ttg gcg ccc cct gag gtg gac	447
Lys Lys Phe Trp Lys Pro Gly Asp Ser Leu Ala Pro Pro Glu Val Asp	
110 115 120	
ttt gac agg ctg ctg gcc agc ctg cag gat ctt agt gag ctg gtg gta	495
Phe Asp Arg Leu Leu Ala Ser Leu Gln Asp Leu Ser Glu Leu Val Val	
125 130 135	
gag ggt gac acc caa gtg aca cca gtg ccc ggc ggg gca cgg ctg cgt	543
Glu Gly Asp Thr Gln Val Thr Pro Val Pro Gly Gly Ala Arg Leu Arg	
140 145 150	
acc ctc gag ccc atc ccg ctg aag ctc tac cgg aat ggc atc atg atg	591
Thr Leu Glu Pro Ile Pro Leu Lys Leu Tyr Arg Asn Gly Ile Met Met	
155 160 165	
ttc gac ggg ccc ttc cag ccc ttc tac gat ccc tcc aca cag cgc tgc	639
Phe Asp Gly Pro Phe Gln Pro Phe Tyr Asp Pro Ser Thr Gln Arg Cys	
170 175 180 185	
ctc cga gac ata ttg gat ggc ttc ttt ccc tca gag ctc cag cga ctg	687
Leu Arg Asp Ile Leu Asp Gly Phe Phe Pro Ser Glu Leu Gln Arg Leu	
190 195 200	
tac ccc aat ggg gtc ccc ttt aag gtg agt gac ttg cgc aat cag gtc	735
Tyr Pro Asn Gly Val Pro Phe Lys Val Ser Asp Leu Arg Asn Gln Val	
205 210 215	
tac ctg gag gat gga ctg gac ccc ttc cca ggc gag ggc cgt gtg gtg	783
Tyr Leu Glu Asp Gly Leu Asp Pro Phe Pro Gly Glu Gly Arg Val Val	
220 225 230	
ggc agg cag cgg atg cac aag gcc ttg gac agg gtg gag gag cac cca	831
Gly Arg Gln Arg Met His Lys Ala Leu Asp Arg Val Glu Glu His Pro	
235 240 245	
ggc tcc agg atg act gct gag aaa ttt ctg aac agg ctc ccc aag ttt	879
Gly Ser Arg Met Thr Ala Glu Lys Phe Leu Asn Arg Leu Pro Lys Phe	
250 255 260 265	
gtg atc cgg caa ggc gag gtg att gac atc cgg ggc ccc atc agg gac	927
Val Ile Arg Gln Gly Glu Val Ile Asp Ile Arg Gly Pro Ile Arg Asp	
270 275 280	
acc ttg cag aac tgc tgc cca ttg cct gcc cgg atc cag gag att gtg	975

Thr Leu Gln Asn Cys Cys Pro Leu Pro Ala Arg Ile Gln Glu Ile Val
285 290 295

gtg gag acg ccc acc ttg gcc gct gag cga gag agg agc cag gag tca 1023
Val Glu Thr Pro Thr Leu Ala Ala Glu Arg Glu Arg Ser Gln Glu Ser
300 305 310

ccc aac aca ccg gca ccc ccg ctc tcc atg ctg cgc atc aag tct gag 1071
Pro Asn Thr Pro Ala Pro Pro Leu Ser Met Leu Arg Ile Lys Ser Glu
315 320 325

aat ggg gaa cag gcc ttc cta ctg atg atg cag cct gac aac acc att 1119
Asn Gly Glu Gln Ala Phe Leu Leu Met Met Gln Pro Asp Asn Thr Ile
330 335 340 345

ggg gac gtg cga gct ctg cta gcg cag gcc agg gtc atg gat gcc tct 1167
Gly Asp Val Arg Ala Leu Leu Ala Gln Ala Arg Val Met Asp Ala Ser
350 355 360

gcc ttt gag atc ttc agc aca ttc ccg ccc acc ctc tac cag gac gat 1215
Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu Tyr Gln Asp Asp
365 370 375

aca ctc acg ctg cag gct gca ggc ctt gtg ccc aaa gca gca ctg ctg 1263
Thr Leu Thr Leu Gln Ala Ala Gly Leu Val Pro Lys Ala Ala Leu Leu
380 385 390

ctg cgg gca cgc cga gcc ccg aag tcc agc ctg aaa ttc agt cct ggt 1311
Leu Arg Ala Arg Arg Ala Pro Lys Ser Ser Leu Lys Phe Ser Pro Gly
395 400 405

ccc tgt ccc ggt ccc ggt ccc ggc ccc agt ccc ggt ccc ggt ccc ggc 1359
Pro Cys Pro Gly Pro Gly Pro Gly Pro Ser Pro Gly Pro Gly Pro Gly
410 415 420 425

tcc agt ccc tgt ccc gga ccc agt ccc agc ccc caa taaagcaccc 1405
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accccctc 1413

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<212> PRT
<213> Homo sapiens

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20 25 30

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Gln	Arg	Gln	Glu	Glu	Leu	Glu	Thr	Met	Cys	Val	Gln	Leu	Gln	Arg	Gln	
	50					55					60					
Val	Arg	Glu	Met	Glu	Arg	Phe	Leu	Ser	Asp	Tyr	Gly	Leu	Gln	Trp	Val	
65					70					75					80	
Gly	Glu	Pro	Met	Asp	Gln	Glu	Asp	Ser	Glu	Ser	Lys	Thr	Val	Ser	Glu	
				85					90					95		
His	Gly	Glu	Arg	Asp	Trp	Met	Thr	Ala	Lys	Lys	Phe	Trp	Lys	Pro	Gly	
			100					105					110			
Asp	Ser	Leu	Ala	Pro	Pro	Glu	Val	Asp	Phe	Asp	Arg	Leu	Leu	Ala	Ser	
		115					120					125				
Leu	Gln	Asp	Leu	Ser	Glu	Leu	Val	Val	Glu	Gly	Asp	Thr	Gln	Val	Thr	
	130					135					140					
Pro	Val	Pro	Gly	Gly	Ala	Arg	Leu	Arg	Thr	Leu	Glu	Pro	Ile	Pro	Leu	
145					150					155					160	
Lys	Leu	Tyr	Arg	Asn	Gly	Ile	Met	Met	Phe	Asp	Gly	Pro	Phe	Gln	Pro	
				165					170					175		
Phe	Tyr	Asp	Pro	Ser	Thr	Gln	Arg	Cys	Leu	Arg	Asp	Ile	Leu	Asp	Gly	
			180					185					190			
Phe	Phe	Pro	Ser	Glu	Leu	Gln	Arg	Leu	Tyr	Pro	Asn	Gly	Val	Pro	Phe	
		195					200					205				
Lys	Val	Ser	Asp	Leu	Arg	Asn	Gln	Val	Tyr	Leu	Glu	Asp	Gly	Leu	Asp	
	210					215					220					
Pro	Phe	Pro	Gly	Glu	Gly	Arg	Val	Val	Gly	Arg	Gln	Arg	Met	His	Lys	
225					230					235					240	
Ala	Leu	Asp	Arg	Val	Glu	Glu	His	Pro	Gly	Ser	Arg	Met	Thr	Ala	Glu	
			245						250					255		
Lys	Phe	Leu	Asn	Arg	Leu	Pro	Lys	Phe	Val	Ile	Arg	Gln	Gly	Glu	Val	

260

265

270

Ile Asp Ile Arg Gly Pro Ile Arg Asp Thr Leu Gln Asn Cys Cys Pro
275280285

Leu Pro Ala Arg Ile Gln Glu Ile Val Val Glu Thr Pro Thr Leu Ala
290295300

Ala Glu Arg Glu Arg Ser Gln Glu Ser Pro Asn Thr Pro Ala Pro Pro
305310315320

Leu Ser Met Leu Arg Ile Lys Ser Glu Asn Gly Glu Gln Ala Phe Leu
325330335

Leu Met Met Gln Pro Asp Asn Thr Ile Gly Asp Val Arg Ala Leu Leu
340345350

Ala Gln Ala Arg Val Met Asp Ala Ser Ala Phe Glu Ile Phe Ser Thr
355360365

Phe Pro Pro Thr Leu Tyr Gln Asp Asp Thr Leu Thr Leu Gln Ala Ala
370375380

Gly Leu Val Pro Lys Ala Ala Leu Leu Leu Arg Ala Arg Arg Ala Pro
385390395400

Lys Ser Ser Leu Lys Phe Ser Pro Gly Pro Cys Pro Gly Pro Gly Pro
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Gly Pro Ser Pro Gly Pro Gly Pro Gly Ser Ser Pro Cys Pro Gly Pro
420425430

Ser Pro Ser Pro Gln
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<210> 4

<211> 20
<212> PRT
<213> Homo sapiens

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Gln Ala Ala Gly
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ggggactcat tggcgcccc tgaggtggac tttgacaggc tgctggccag cctgcaggat 180
cttagtgagc tgggtggtaga gggtgacacc caagtgacac cagtgcccgg cggggcacgg 240
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gacttgcgca atcaggtcta cctggaggat ggactggacc ccttcccagg cgagggccgt 480
gtgggtgggca ggcagcggat gcacaaggcc ttggacaggg tggaggagca cccaggctcc 540

aggatgactg ctgagaaatt tctgaacagg ctccccaagt tttgatccgg caaggcgagg 600
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ggatccagga gattgtggtg gagacgcca ccttggccgc tgagcgagag aggagccagg 720
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ccctctacca ggacgataca ctcacgctgc aggctgcagg ccttgtgccc aaagcagcac 960
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35 40 45

Val Asp Phe Asp Arg Leu Leu Ala Ser Leu Gln Asp Leu Ser Glu Leu
50 55 60

Val Val Glu Gly Asp Thr Gln Val Thr Pro Val Pro Gly Gly Ala Arg
65 70 75 80

Leu Arg Thr Leu Glu Pro Ile Pro Leu Lys Leu Tyr Arg Asn Gly Ile
85 90 95

Met Met Phe Asp Gly Pro Phe Gln Pro Phe Tyr Asp Pro Ser Thr Gln
100 105 110

Arg Cys Leu Arg Asp Ile Leu Asp Gly Phe Phe Pro Ser Glu Leu Gln
115 120 125

Arg Leu Tyr Pro Asn Gly Val Pro Phe Lys Val Ser Asp Leu Arg Asn
130 135 140

Gln Val Tyr Leu Glu Asp Gly Leu Asp Pro Phe Pro Gly Glu Gly Arg
145 150 155 160

Val Val Gly Arg Gln Arg Met His Lys Ala Leu Asp Arg Val Glu Glu
165 170 175

His Pro Gly Ser Arg Met Thr Ala Glu Lys Phe Leu Asn Arg Leu Pro
180 185 190

Lys Phe Val Ile Arg Gln Gly Glu Val Ile Asp Ile Arg Gly Pro Ile
195 200 205

Arg Asp Thr Leu Gln Asn Cys Cys Pro Leu Pro Ala Arg Ile Gln Glu
210 215 220

Ile Val Val Glu Thr Pro Thr Leu Ala Ala Glu Arg Glu Arg Ser Gln
225 230 235 240

Glu Ser Pro Asn Thr Pro Ala Pro Pro Leu Ser Met Leu Arg Ile Lys
245 250 255

Ser Glu Asn Gly Glu Gln Ala Phe Leu Leu Met Met Gln Pro Asp Asn
260 265 270

Thr Ile Gly Asp Val Arg Ala Leu Leu Ala Gln Ala Arg Val Met Asp
275 280 285

Ala Ser Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu Tyr Gln
290 295 300

Asp Asp Thr Leu Thr Leu Gln Ala Ala Gly Leu Val Pro Lys Ala Ala
305 310 315 320

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Pro Gly Pro Cys Pro Gly Pro
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<210> 10
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cttgtgcca aagcagcact gctgctgcgg gcacgccgag cccgaagtc cagcctgaaa 180
ttcagtcctg gtccctgtcc cgggtcccggc cccggcccca gtcccgggtcc cgggtcccggc 240
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20 25 30

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35 40 45

Leu Arg Ala Arg Arg Ala Pro Lys Ser Ser Leu Lys Phe Ser Pro Gly
50 55 60

Pro Cys Pro Gly Pro Gly Pro Gly Pro Ser Pro Gly Pro Gly Pro Gly
65 70 75 80

Ser Ser Pro Cys Pro Gly Pro Ser Pro Ser Pro Gln
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